bio-protocol Preprint

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Assessment of CpG methylation status by bisulfite sequencing

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An abbreviated version of this protocol was published in eLIFE in Sep 2013

DNA methylation presents distinct binding sites for human transcription factors

DOI: 10.7554/eLife.00726

Detailed protocol

Assessment of CpG methylation status by bisulfite sequencing

1. Purified genomic DNA or ChIP DNA from H1 cells and treated by EZ DNA Methylation-Direct Kit (Zymo Research, Irvine, CA) for bisulfite conversion.
2. After bisulfite conversion, regions of interest were PCR-amplified. The primers were listed in Supplementary file 1E.
3. PCR products were gel-purified and cloned into a TA vector (Life Technologies).
4. Individual clones were Sanger sequenced and aligned with the reference sequence.

How to cite:（Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used）

1. Su, Y. (2020). Assessment of CpG methylation status by bisulfite sequencing. Bio-protocol Preprint. bio-protocol.org/prep568.
2. Hu, S., Wan, J., Su, Y., Song, Q., Zeng, Y., Nguyen, H. N., Shin, J., Cox, E., Rho, H. S., Woodard, C., Xia, S., Liu, S., Lyu, H., Ming, G., Wade, H., Song, H., Qian, J. and Zhu, H.(2013). DNA methylation presents distinct binding sites for human transcription factors. eLIFE. DOI: 10.7554/eLife.00726

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